



QY 241 GGGCTGGCGTCGACATGATTCGCCAGAAAGATGGCGGCCGCGCTCTCTTGGC 300  
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 Db 301 GGTCCGCGCCGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
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 Db 361 AAGGTCCCTTCTCTCTATGATGATGATGATGATGATGATGATGATGATGATG 420  
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 Db 421 GAGTGTGATGAGAAATTTCCGTAGAGCTATAGCTTATAGCTTATAGCTTATAG 480  
 QY 481 GTTATGAGAGAGAGGTTAGTGAACCTTCCCGAGAGAGAGAGAGAGAGAGAGAG 540  
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 QY 541 TATGCAAAAAGCATTAGCATGATGATGATGATGATGATGATGATGATGATGATG 600  
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 Db 601 CTGAGTGTAGATTTCTCAATTTATGATGATGATGATGATGATGATGATGATGAT 660  
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 Db 661 GTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
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 Db 841 CCACAGGTGCGCAAGATATTTTGTCTTATGAGGCCAGATGATGATGATGATGATG 900  
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 DEFINITION Sequence 9 from Patent WO0105975.  
 ACCESSION AX077232  
 VERSION AX077232.1 GI:13121826  
 KEYWORDS  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 1869)  
 AUTHORS Mahajan, P.B.  
 TITLE Maize orthologues of bacterial ruvB:cdnas and uses thereof  
 JOURNAL Patent: WO 0105975-A 9 25-JAN-2001.  
 PIONEER HI-BRED INTERNATIONAL, INC. (US)  
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BASE COUNT 539 a 373 c 486 g 471 t  
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Query Match 56.5%; Score 1080; DB 6; Length 1869;  
 Best Local Similarity 99.9%; Pred. No. 0;  
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397 TACTCTCGAGAGTCAAGAACTGAGTGTGATGGAATTTCCGTAGAGCTTAGGT 456  
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 Db 316 TACTCTCGAGAGTCAAGAACTGAGTGTGATGGAATTTCCGTAGAGCTTAGGT 375

457 TTGCGATTAAGAAACAAGAGGTTTATGAAGAGAGGTTACTGAACTTCCACAGAA 516  
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 Db 376 TTGCGATTAAGAAACAAGAGGTTTATGAAGAGAGGTTACTGAACTTCCACAGAA 435

517 GAGGCTGAGAGTCAACAGTGGTATGCAAAAGCATTAGCATATATCATAGCTTA 576  
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 Db 436 GAGGCTGAGAGTCAACAGTGGTATGCAAAAGCATTAGCATATATCATAGCTTA 495

577 AAGACTGTTAAGAGGAGTCAAGCACTGAAGTATGATTTCTCAATTTATGATGCTTGATC 636  
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1117 GATATGACAACTCCATGATATACCGGTGATCTTCTAGATAGGCTGTTGATATTCGG 1176  
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 Db 1336 TCGGCTGGCTGCTGCTCAGAGCAACAAGAAAGATATCATCACTAGATTGG 1386

## RESULT 3

AX077224 1845 bp DNA linear PAT 22-FEB-2001  
 LOCUS  
 DEFINITION Sequence 1 from Patent WO0105975.  
 ACCESSION AX077224  
 VERSION AX077224.1 GI:13121818  
 KEYWORDS  
 SOURCE  
 ORGANISM

Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoidae; Andropogoneae; Zea.  
 1 (bases 1 to 1845)

REFERENCE  
 AUTHORS Mahajan, P.B.  
 TITLE Maize orthologues of bacterial ruvB:cdnas and uses thereof  
 JOURNAL Patent: WO 0105975-A 1 25-JAN-2001;  
 PIONEER HI-BRED INTERNATIONAL, INC. (US)

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 ERIT"

BASE COUNT 530 a 378 c 490 g 445 t 2 others  
 ORIGIN

Query Match 30.1%; Score 576; DB 6; Length 1845;  
 Best Local Similarity 98.8%; Pred. No. 0;

Matches 1426; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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 Db 75 GTTGGGGCCATGAGATGAGAGGTCAGCTGACCTGGAAGCAACAGCATGCCAC 134

Qy 144 CCACACCCATCAAGGAGCTGCGCTCGACGCCAATGGGATGGCGATTGGCGCGC 203  
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 Db 135 CCACACCCATCAAGGAGCTGCGCTCGACGCCAATGGGATGGCGATTGGCGCGC 194

Qy 204 GGGGTTGCTGGCGCAGGCGCGCGCGCGAGGCGCGGAGCTGGCGTGCATGATTCG 263  
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Qy 264 CCAGAAGAAAGATGCGCGCGCGCGCGGTCCTTGGGGTCCGCGCGCAGCGGCAAGAC 323  
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 Db 255 CCAGAAGAAAGATGCGCGCGCGCGCGGTCCTTGGGGTCCGCGCGCAGCGGCAAGAC 314

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Db 1515 GTG 1517

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Job time : 3390 secs

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 06:14:52 ; Search time 2048 seconds

(without alignments)  
15120.005 Million cell updates/sec

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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 100

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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7: em\_estro:\*  
8: em\_hlc:\*  
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13: gb\_est4:\*  
14: gb\_est5:\*  
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24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	298	15.6	474	10	BE512426 BE512426
5	248	13.0	248	10	BE512215 946066A01
6	134	7.0	549	10	BE512425 946071A06

c	7	113	5.9	318	14	BM736925
c	8	110	5.8	375	10	BE640273
c	9	109	5.7	109	12	BG316941

## ALIGNMENTS

RESULT 1  
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LOCUS 612 bp mRNA linear EST 01-MAR-2002  
DEFINITION 952050H12.xl 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea  
mays cDNA, mRNA sequence.  
ACCESSION BM736448  
VERSION BM736448.1 GI:19057781  
KEYWORDS EST.  
SOURCE Zea mays.  
ORGANISM Zea mays.  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 612)  
Walbot, V.  
Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 952050 row: H column: 12.  
Location/Qualifiers  
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library was prepared by George Rudenko using poly (A)  
selected RNA and Universal Riboclone cDNA Synthesis System  
(Promega). cDNA was synthesized using both random and  
oligo(dT) primers in separate reactions and equipped with  
EcoRI adaptors. Library was size-fractionated on agarose  
gels (for insert size >400bp) and non-directionally cloned  
into EcoRI-digested pUC19 vector. Blue/white selection on  
carbenicillin-containing plates was used to recover  
positive clones."

## FEATURES

source

BASE COUNT 159 a 143 c 199 g 111 t  
ORIGIN  
Query Match 26.7% Score 510, DB 14, Length 612;  
Best Local Similarity 99.7% Pred. No. 6, 4e-122;  
Matches 610; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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QY 222 GCGCGCGCGGAGCGCGCGCGCTGGCTGCATGATGTCGCCAGAGAGATGCGCG 281  
 DB 181 GCGCGCGCGGAGCGCGCGCGCGCTGGCTGCATGATGTCGCCAGAGAGATGCGCG 240  
 QY 282 CCGCGCGCTGCTCTTCCGCGGCTCCCGCCGACGCGGCAAGCGCGCTGCGCGCAT 341  
 DB 241 CCGCGCGCTGCTCTTCCGCGGCTCCCGCCGACGCGGCAAGCGCGCTGCGCGCAT 300  
 QY 342 AGCCGAGGAGCTGGGAGGAGAGGTCCTTCTGCTATGATGATGATGATGATGATC 401  
 DB 301 AGCCGAGGAGCTGGGAGGAGAGGTCCTTCTGCTATGATGATGATGATGATGATC 360  
 QY 402 CTCGAGAGCTGAGAGAGAGAGGTCGCTGATGAGAGAGAGAGAGAGAGAGAGAGG 461  
 DB 361 CTCGAGAGCTGAGAGAGAGAGGTCGCTGATGAGAGAGAGAGAGAGAGAGAGAGG 420  
 QY 462 TATTAAGG 521  
 DB 421 TATTAAGG 480  
 QY 522 TGAGAGTACAGG 581  
 DB 481 TGAGAGTACAGG 540  
 QY 582 TGTAAAGGAGCTAGG 641  
 DB 541 TGTAAAGGAGCTAGG 600  
 QY - 642 AAAGTGGCAGT 653  
 DB 601 AAAGTGGCAGT 612

RESULT 2  
 BE512278 610 bp mRNA linear EST 07-AUG-2000  
 LOCUS BE512278 946066D09.y1 946 - tassal primordium prepared by Schmidt lab Zea  
 DEFINITION mays cDNA, mRNA sequence.  
 ACCESSION BE512278  
 VERSION BE512278.1 GI:9733421  
 KEYWORDS EST.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoidae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 610)  
 AUTHORS Walbot, V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford  
 UNIVERSITY  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 946066 row: D column: 09.  
 FEATURES  
 Source  
 1. 610  
 Location/Qualifiers  
 /organism="Zea mays"  
 /cultivar="OH43"  
 /db\_xref="taxon:4577"  
 /clone\_id="946 - tassal primordium prepared by Schmidt  
 lab"  
 /tissue\_type="tassels"  
 /dev\_stage="just after the transition from vegetative to  
 inflorescence development"  
 /lab\_host="XLOLR"  
 /note="Organ: tassels; Vector: HybriLAP; Site\_1: EcorI;  
 Site\_2: XhoI; George Chuck dissected immature tassels

BASE COUNT 160 a 135 c 196 g 119 t  
 ORIGIN  
 Query Match 21.1%; Score 403; DB 10; Length 610;  
 Best Local Similarity 99.5%; Pred. No. 1.8e-94;  
 Matches 553; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 between 1mm and 3mm. Sharon Stanfield prepared the cDNA  
 library in HybriLAP. Sample insert size range was 350 bp  
 to 3 kb with a 1 kb average.

QY 116 CGACCTCAGG 175  
 DB 31 CGACCTCAGG 90  
 QY 176 CCAATGGAGATGGCGATGCTGGGCGGCGGCTGCTGAGGCGGCGGCGGCGGAGG 235  
 DB 91 CCAATGGAGATGGCGATGCTGGGCGGCGGCTGCTGAGGCGGCGGCGGCGGAGG 150  
 QY 236 CCGCGGCGCTGGCGCTGCATGATGTCGCCAGAGAGATGCGCGCGCGCTGCTCC 295  
 DB 151 CCGCGGCGCTGGCGCTGCATGATGTCGCCAGAGAGATGCGCGCGCGCTGCTCC 210  
 QY 296 TTGCGGCTCCCGCCCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 355  
 DB 211 TTGCGGCTCCCGCCCGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGG 270  
 QY 356 GCAGCAGAGTCCCTTCTGCTATGATGATGATGATGATGATGATGATGATGATGATG 415  
 DB 271 GCAGCAGAGTCCCTTCTGCTATGATGATGATGATGATGATGATGATGATGATGATG 330  
 QY 416 AAACGTAGAGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 475  
 DB 331 AAACGTAGAGTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 390  
 QY 476 AAGAGTTATAGG 535  
 DB 391 AAGAGTTATAGG 450  
 QY 536 GTGATATGCAAAAGG 595  
 DB 451 GTGATATGCAAAAGG 510  
 QY 596 AGCACTGAGAGTTAGATTTCTCAATTATGATGCTGTGATGATGATGATGATGATG 655  
 DB 511 AGCACTGAGAGTTAGATTTCTCAATTATGATGCTGTGATGATGATGATGATGATG 570  
 QY 656 GTGATATATATCAT 671  
 DB 571 GTGATATATATCAT 586

RESULT 3  
 AY109398 1542 bp mRNA linear HTC 25-MAY-2002  
 LOCUS AY109398 1542 bp mRNA linear HTC 25-MAY-2002  
 DEFINITION Zea mays CL5641\_1 mRNA sequence.  
 ACCESSION AY109398  
 VERSION AY109398.1 GI:21213108  
 KEYWORDS HTC.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoidae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 1542)  
 AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,  
 Arthur, L.W., Hanefey, M., Morgante, M., and Tingey, S.V.  
 TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of  
 Overgo Probes  
 JOURNAL Unpublished (2002)  
 REFERENCE 2 (bases 1 to 1542)  
 AUTHORS Coe, E.C.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of



REFERENCE 1 (bases 1 to 248)  
 AUTHOR Walbot, V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
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 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 946066 row: A column: 01.

FEATURES  
 source  
 1..248  
 /organism="Zea mays"  
 /cultivar="OH43"  
 /db\_xref="taxon:4577"  
 /clone\_id="946 - tassal primordium prepared by Schmidt lab"  
 /issue\_type="tassels"  
 /dev\_stage="just after the transition from vegetative to inflorescence development"  
 /lab\_host="XLOLR"  
 /note="Organ: tassels; Vector: HybridAP; Site\_1: EcoRI; Site\_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridAP. Sample insert size range was 350 bp to 3 kb with a 1 kb average."

BASE COUNT  
 ORIGIN 87 a 37 c 63 g 61 t

Query Match  
 Best Local Similarity 13.0%; Score 248; DB 10; Length 248;  
 Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 399 CTCCTCGAGGTCAAGAACTGAGTGCATGAGGAAATTTCCGTAGACTTATAGTTT 458  
 Db 1 CTCCTCGAGGTCAAGAACTGAGTGCATGAGGAAATTTCCGTAGACTTATAGTTT 60  
 QY 459 GCGTATTAAGGAAACAAAGAGTTTATGAAGAGAGAGTACTGAACCTTCCCCAGAGA 518  
 Db 61 GCGTATTAAGGAAACAAAGAGTTTATGAAGAGAGAGTACTGAACCTTCCCCAGAGA 120  
 QY 519 GCGTGAAGATACACTGTGTGATATGCAAAAAGCATTTAGCCATTAATCATCAGCTTAA 578  
 Db 121 GCGTGAAGATACACTGTGTGATATGCAAAAAGCATTTAGCCATTAATCATCAGCTTAA 180  
 QY 579 GACTGTAAAGGAGACTGAACACTGAATGTATCTCAATTTATGATGCTGTATCA 638  
 Db 181 GACTGTAAAGGAGACTGAACACTGAATGTATCTCAATTTATGATGCTGTATCA 240  
 QY 639 GGAAGAG 646  
 Db 241 GGAAGAG 248

RESULT 6  
 BE512425/c 549 bp mRNA linear EST 07-AUG-2000  
 LOCUS 946071A06.x1 946 - tassal primordium prepared by Schmidt lab Zea  
 DEFINITION mays cDNA, mRNA sequence.  
 ACCESSION BE512425  
 VERSION BE512425.1 GI:9733673  
 KEYWORDS EST.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 549)  
 AUTHORS Walbot, V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford

JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V  
 Department of Biological Sciences  
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 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Plate: 946071 row: A column: 06.

FEATURES  
 source  
 1..549  
 /organism="Zea mays"  
 /cultivar="OH43"  
 /db\_xref="taxon:4577"  
 /clone\_id="946 - tassal primordium prepared by Schmidt lab"  
 /issue\_type="tassels"  
 /dev\_stage="just after the transition from vegetative to inflorescence development"  
 /lab\_host="XLOLR"  
 /note="Organ: tassels; Vector: HybridAP; Site\_1: EcoRI; Site\_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybridAP. Sample insert size range was 350 bp to 3 kb with a 1 kb average."

BASE COUNT  
 ORIGIN 150 a 146 c 116 g 137 t

Query Match  
 Best Local Similarity 7.0%; Score 134; DB 10; Length 549;  
 Matches 284; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1240 ATTGATATGATGAAGAAAGTCTTCTTATTTAGGCGAGATCGACACAGATCTTTG 1299  
 Db 519 ATTGATATGATGAAGAAAGTCTTCTTATTTAGGCGAGATCGACACAGATCTTTA 460  
 QY 1300 AGACATGCTATTCATTTGATATACCTGCGAGCGTGGTCTCAAGAGCTAATGGAAGAG 1359  
 Db 459 AGACATGCTATTCATTTGATATACCTGCGAGCGTGGTCTCAAGAGCTAATGGAAGAG 400  
 QY 1360 AAAATCTGCAAGCGTATCTCGAGAGTCAAGTGGCTTATTTGGATGCCAAATCTCG 1419  
 Db 399 AAAATATGCAAGCGTATCTCGAGAGTCAAGTGGCTTATTTGGATGCCAAATCTCG 340  
 QY 1420 GCTCGGCTGCTCAGAGACCAAGAAAGATACATCACCTAGATTGATCTCTGCTG 1479  
 Db 339 GCTCGGCTGCTCAGAGACCAAGAAAGATACATCACCTAGATTGATCTCTGCTG 280  
 QY 1480 GGAAGTCTCGAAGAGATGATTGCCAGTCAAGATCATCTAGTG 1526  
 Db 279 GGAAGTCTCGAAGAGATGATTGCCAGTCAAGATCATCTAGTG 233

RESULT 7  
 BM736925/c 318 bp mRNA linear EST 01-MAR-2002  
 LOCUS 952050H12.y1 952 - BMS tissue from Walbot Lab (reduced rRNA) Zea  
 DEFINITION mays cDNA, mRNA sequence.  
 ACCESSION BM736925  
 VERSION BM736925.1 GI:19058258  
 KEYWORDS EST.  
 SOURCE Zea mays.  
 ORGANISM Zea mays.  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC  
 clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 318)  
 AUTHORS Walbot, V.  
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Walbot V



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Plate: 952050 row: H column: 12.

location/Qualifiers  
1. .318

## FEATURES

source

/organism="Zea mays"  
/cultivar="BMS (Black Mexican Sweet)"  
/db\_xref="taxon:4577"  
/clone\_lib="952 - BMS tissue from Walbot Lab (reduced RNA)"  
/tissue\_type="suspension culture"  
/dev\_stage="mixed logarithmic and stationary growth phases"  
/lab\_host="DH10B"  
/note="Vector: pUC19; Site\_1: EcoRI; Site\_2: EcoRI; The library was prepared by George Rudenko using poly (A) selected RNA and Universal Riboclone cDNA Synthesis System (Promega). cDNA was synthesized using both random and oligo(dT) primers in separate reactions and equipped with EcoRI adaptors. Library was size-fractionated on agarose gels (for insert size >400bp) and non-directionally cloned into EcoRI-digested pUC19 vector. Blue/white selection on carbenicillin-containing plates was used to recover positive clones."

BASE COUNT 86 a 78 c 62 g 92 t  
ORIGIN

Query Match 5.9%; Score 113; DB 14; Length 318;  
Best Local Similarity 99.4%; Pred. No. 8.8e-20;

Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1042 CTGTCATTGGAGAGCCCATATATACCATGTCATCTCTCAAAATAGGGAATATGT 1101

DB 318 CTGTCATTGGAGAGCCCATATATACCATGTCATCTCTCAAAATAGGGAATATGT 259

QY 1102 AATGTAGAGAACTGATATATGACAGTCATGATACCGGTGATCTTCTAGATAGG 1161

DB 258 AATGTAGAGAACTGATATGACAGTCATGATACCGGTGATCTTCTAGATAGG 199

QY 1162 CTGGTATTATTCGAGACAGACATATGCCCCCTACTGAGATGAT 1205

DB 198 CTGGTATTATTCGAGACAGACATATGCCCCCTACTGAGATGAT 155

RESULT 8 BE640273 375 bp mRNA linear EST 30-AUG-2000

LOCUS BE640273.1 946082B06.x1 946 - tassal primordium prepared by Schmidt lab Zea

DEFINITION mays cDNA, mRNA sequence.

ACCESSION BE640273

VERSION BE640273.1

KEYWORDS GT:953690

SOURCE Zea mays.

ORGANISM Zea mays.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

TITLE clade; Panicoidae; Andropogoneae; Zea.

JOURNAL 1 (bases 1 to 375)

COMMENT Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford

Plate: 946082 row: B column: 06.

## FEATURES

source

location/Qualifiers  
1. .375  
/organism="Zea mays"  
/cultivar="OH43"  
/db\_xref="taxon:4577"  
/clone\_lib="946 - tassal primordium prepared by Schmidt lab"  
/tissue\_type="tassels"  
/dev\_stage="just after the transition from vegetative to inflorescence development"  
/lab\_host="XLOLR"  
/note="Organ: tassels; Vector: HybrizAP; Site\_1: EcoRI; Site\_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybrizAP. Sample insert size range was 350 bp to 3 kb with a 1 kb average."

BASE COUNT 106 a 106 c 79 g 84 t  
ORIGIN

Query Match 5.8%; Score 110; DB 10; Length 375;

Best Local Similarity 99.4%; Pred. No. 4.4e-19;

Matches 160; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1366 TCGAAGGCTGATCTGAGAGTCAGTGGCTCTATTGGATGCCAAATCCGCGCTCGG 1425

DB 364 TCGAAGGCTGATCTGAGAGTCAGTGGCTCTATTGGATGCCAAATCCGCGCTCGG 305

QY 1426 CTGCTCCAGAGCAACAGAAAGATACATCACCTGATTTGGATCTCTGCTGGAAGT 1485

DB 304 CTGCTCCAGAGCAACAGAAAGATACATCACCTGATTTGGATCTCTGCTGGAAGT 245

QY 1486 CTCGAAGAAGATGTAGTTCGCCAGCTCGAAAGTCATCTGCTG 1526

DB 244 CTCGAAGAAGATGTAGTTCGCCAGCTCGAAAGTCATCTGCTG 204

RESULT 9 BG316941 109 bp mRNA linear EST 26-FEB-2001

LOCUS 947024C05.x2 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA

DEFINITION sequence.

ACCESSION BG316941

VERSION BG316941.1

KEYWORDS GT:13126371

SOURCE Zea mays.

ORGANISM Zea mays.

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC

TITLE clade; Panicoidae; Andropogoneae; Zea.

JOURNAL 1 (bases 1 to 109)

COMMENT Walbot, V.

Maize ESTs from various cDNA libraries sequenced at Stanford

University

unpublished (1999)

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Email: walbot@stanford.edu

Plate: 947024 row: C column: 05.

location/Qualifiers

1. .109

/organism="Zea mays"

/cultivar="B73"

/db\_xref="taxon:4577"

/clone\_lib="947 - 2 week shoot from Barkan lab"

/tissue\_type="leaf and stem, including leaf base"

/dev\_stage="2 week old seedling (3 leaves)"

/lab\_host="XLI-Blue"

/note="Organ: shoot; Vector: Lambda ZAP (pBluescript SK-);

Site\_1: EcoRI; Site\_2: XhoI; Directionally cloned using  
Stratagene's Unizap XR cDNA cloning kit with the 5' end  
at the EcoRI site. The library represents 8 x 10<sup>5</sup>  
independent recombinant phage. The plants were greenhouse  
grown."

BASE COUNT 30 a 29 c 17 g 33 t  
ORIGIN

Query Match 5.7%; Score 109; DB 12; Length 109;  
Best Local Similarity 100.0%; Pred. No. 2.5e-18;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1214 TGGCTATCCGACGACAAGTGGAGAGATGATGATGAAGAAAGTCTGCTATTAG 1273  
|||||  
Db 109 TGGCTATCCGACGACAAGTGGAGAGATGATGATGAAGAAAGTCTGCTATTAG 50

OY 1274 GCGAGATGAGACAGACATCTTTGAGACATGCTATTCAATTGATATC 1322  
|||||  
Db 49 GCGAGATGAGACAGACATCTTTGAGACATGCTATTCAATTGATATC 1

Search completed: December 5, 2002, 07:53:46  
Job time : 2058 secs

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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 06:20:01 ; Search time 73 Seconds  
(without alignments)  
10213.033 Million cell updates/sec

Title: US-09-589-510-3  
Perfect score: 1912  
Sequence: 1 acccacgcgtccgcaattt.....aaaaaaaaaaaaaaaaaaaa 1912

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 350425 seqs, 194966369 residues

Word size : 100

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published\_Applications\_NA:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

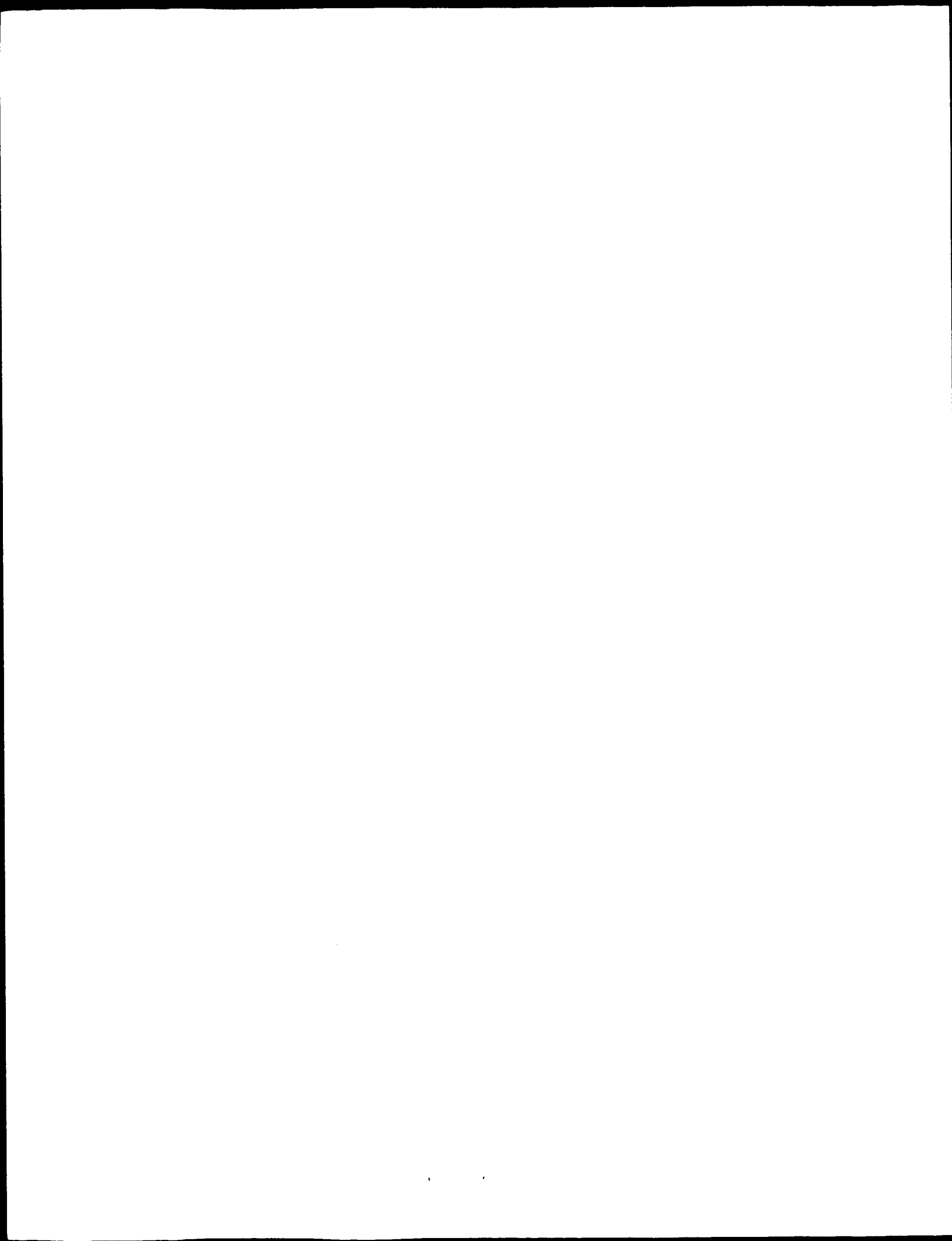
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
-----					

No matches found

Search completed: December 5, 2002, 07:55:17  
Job time : 76 secs



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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 04:53:19 ; Search time 66 Seconds  
(without alignments)  
8884.333 Million cell updates/sec

Title: US-09-589-510-3  
Perfect score: 1912  
Sequence: 1 acccacgcgtccgcaattt.....aaaaaaaaaaaaaaaaaaaa 1912

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 100

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

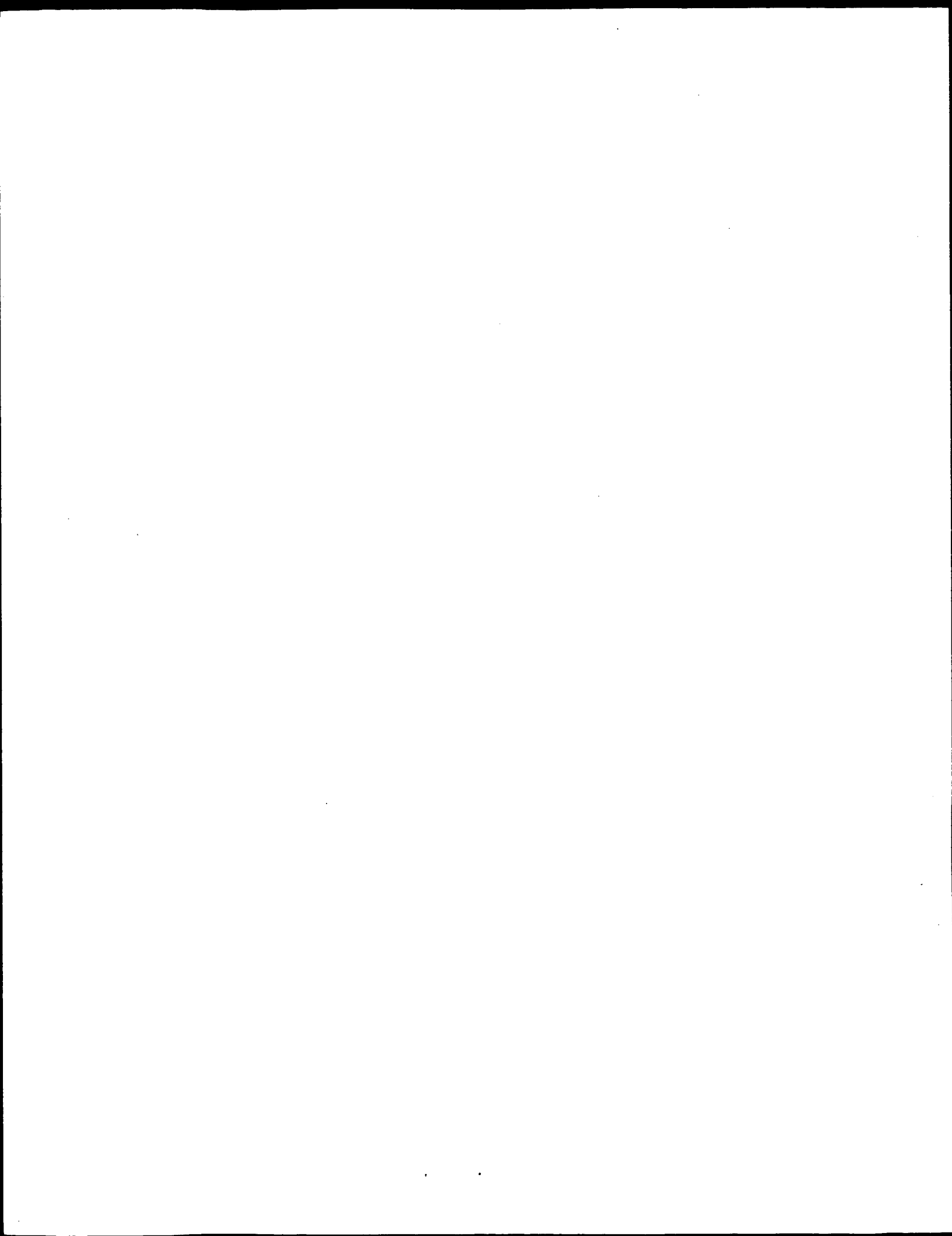
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
- and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
-----					

No matches found

Search completed: December 5, 2002, 06:21:18  
Job time : 71 secs



GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2002, 04:52:00 ; Search time 283 Seconds  
(without alignments)  
15214.914 Million cell updates/sec

Title: US-09-589-510-3

Perfect score: 1912

Sequence: 1 accacgcgtcgcaattt.....aaaaaaaaaaaaaaaaaaaa 1912

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

Word size : 100

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

N\_Geneseq\_l01002:\*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1980.DAT:\*

2: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*

3: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1982.DAT:\*

4: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1983.DAT:\*

5: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1984.DAT:\*

6: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1985.DAT:\*

7: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1986.DAT:\*

8: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1987.DAT:\*

9: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1988.DAT:\*

10: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1989.DAT:\*

11: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1990.DAT:\*

12: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1991.DAT:\*

13: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1992.DAT:\*

14: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1993.DAT:\*

15: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1994.DAT:\*

16: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1995.DAT:\*

17: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1996.DAT:\*

18: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1997.DAT:\*

19: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1998.DAT:\*

20: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA1999.DAT:\*

21: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:\*

22: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT:\*

23: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT:\*

24: /SIDS2/gcgdata/geneseq/geneseq-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1912	100.0	1912	22	Maize RuvB ortholo
2	1080	56.5	1869	22	Maize RuvB ortholo
3	576	30.1	1845	22	Maize RuvB ortholo

#### ALIGNMENTS

RESULT 1

AAD02567

ID AAD02567 standard; cDNA; 1912 BP.

XX

AC AAD02567;

XX

DT 02-MAY-2001 (first entry)

XX

DE Maize RuvB orthologue #2 cDNA.

XX

KW Maize; RuvB orthologue; branch migration; heteroduplex extension; homologous recombination; transposition; transgenic plant; ss.

XX

OS Zea mays.

XX

FH Key Location/Qualifiers

FT CDS 94..1461

FT /\*tag= a

FT /product= "Maize RuvB orthologue protein #2"

XX

PN WO200105975-A1.

XX

PD 25-JAN-2001.

XX

PF 13-JUN-2000; 2000WO-US16271.

XX

PR 16-JUL-1999; 99US-0144112.

XX

PA (PION-) PIONEER HI-BRED INT INC.

XX

PI Mahajan PB;

XX

DR WPI: 2001-159537/16.

DR P-PSDB; AAY72563.

XX

PT Novel maize RuvB nucleic acid useful for modulating levels of maize RuvB in plants, as probes or amplification primers in the detection, quantitation or isolation of gene transcripts -

PT

PS Claim 1; Page 70-72; 87pp; English.

XX

CC The present sequence is a Zea mays RuvB orthologue #2 cDNA. RuvB along with RuvA catalyses the branch migration process, also known as heteroduplex extension, in homologous recombination. RuvB is used for the control of homologous recombination or transposition efficiency in transgenic plants. The RuvB nucleotide may be used as probes or amplification primers for detecting, quantifying or isolating gene transcripts, in detecting deficiencies in the mRNA level during screening for desired transgenic plants, for detecting gene mutations, for monitoring upregulation of expression or changes in enzyme activity, for detecting any number of allelic variants, orthologues or paralogues of the gene, or for site directed mutagenesis in eukaryotic cells. It may also be used for recombinant expression of its encoded polypeptide, or for use as immunogen in preparing and/or screening of antibodies, and in sense or antisense suppression of one or more genes in a host cell, tissue or plant. The RuvB proteins may be used in assays to agonise or antagonise the enzyme function, or as immunogens or antigens for screening antibodies.

XX

Sequence 1912 BP; 547 A; 385 C; 515 G; 462 T; 3 other;

XX

Query Match 100.0%; Score 1912; DB 22; Length 1912;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1912; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCACACGGTCCGCAAAATTTGTCGGCGGGAGAGCCGGAGAGGAGCGTCCACAGAA 60

|||||

Db 1 ACCACACGGTCCGCAAAATTTGTCGGCGGGAGAGCCGGAGAGGAGCGTCCACAGAA 60

|||||

QY 61 ACAGAGAGCGCATACCGCGCGCTTGGCGGGATGAGATCGAGGAGTGCAGTCGACC 120

|||||

Db 61 ACAGAGAGCGCATACCGCGCGCTTGGCGGGATGAGATCGAGGAGTGCAGTCGACC 120

|||||

QY 121 TCGAAGAAGCAGCGCATCGCCACCCACACATCAAGGGACTCGGCTCGACGCCAAT 180

Db 121 TCGAAGAGCAGCGCATCGCCACCCACACACATCAAGGGAAGTCTCGACGCCAAT 180  
 QY 181 GGGATGCGGATTCGGTGGCGGGGGTTCGTGGCCAGCGCGCGCGCGCGCGCGCC 240  
 Db 181 GGGATGCGGATTCGGTGGCGGGGGTTCGTGGCCAGCGCGCGCGCGCGCGCGCC 240  
 QY 241 GGGCTGGCGGTTCGACATGATTCGCCAAGAAAGATGGCGCGCGCGCGCGCGCGCG 300  
 Db 241 GGGCTGGCGGTTCGACATGATTCGCCAAGAAAGATGGCGCGCGCGCGCGCGCGCG 300  
 QY 301 GGTCCG 360  
 Db 301 GGTCCG 360  
 QY 361 AAGTCCCTTCCTGCTCTATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 Db 361 AAGTCCCTTCCTGCTCTATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 QY 421 GAGTGTGATGAAATTTCCGCTAGAGCTATAGGTTTGGCTATAAGGAAACAAAGAG 480  
 Db 421 GAGTGTGATGAAATTTCCGCTAGAGCTATAGGTTTGGCTATAAGGAAACAAAGAG 480  
 QY 481 GTTATGAAGGAGGTTACTGAATTTCCGCTAGAGCTATAGGTTTGGCTATAAGGAG 540  
 Db 481 GTTATGAAGGAGGTTACTGAATTTCCGCTAGAGCTATAGGTTTGGCTATAAGGAG 540  
 QY 541 TATCAAAAGAGCATAGCCATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 Db 541 TATCAAAAGAGCATAGCCATGATGATGATGATGATGATGATGATGATGATGATGAT 600  
 QY 601 CTGAAGTTAGATTTCAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 Db 601 CTGAAGTTAGATTTCAATTTATGATGATGATGATGATGATGATGATGATGATGATGAT 660  
 QY 661 GTTATATACATGAAAGATAGTGGAGCAGTGAAGAGTGGTGAATGATGATGATGATGAT 720  
 Db 661 GTTATATACATGAAAGATAGTGGAGCAGTGAAGAGTGGTGAATGATGATGATGATGAT 720  
 QY 721 GCTACAGATACGATTTGAAGCTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 780  
 Db 721 GCTACAGATACGATTTGAAGCTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGT 780  
 QY 781 AAGAAAAAGAAATTTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAG 840  
 Db 781 AAGAAAAAGAAATTTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAGTGTGAGGAG 840  
 QY 841 CCACAGGTGGCCAGATATTTGTCCTTATGGCCAGATGATGAACACCAAGAGACT 900  
 Db 841 CCACAGGTGGCCAGATATTTGTCCTTATGGCCAGATGATGAACACCAAGAGACT 900  
 QY 901 GAAATACCGAAAACTACGCCAAGAAATTAAGTGGTGAATATGATATCGATGAA 960  
 Db 901 GAAATACCGAAAACTACGCCAAGAAATTAAGTGGTGAATATGATATCGATGAA 960  
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 Db 961 GGAATTCAGAGCTGTACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1020  
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 Db 1021 GAATGTTTTCTTATCTTAACCGTGCATTCGAGAGCCCATATCACCATCGTATCCT 1080  
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 QY 1141 CCGGTGGATCTTCATAGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1200  
 Db 1141 CCGGTGGATCTTCATAGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1200  
 QY 1201 ATGATACAGATATTTGGCTATCCGAGCACAAGTGGAGGAGATGATGATGATGATGATGAT 1260  
 Db 1201 ATGATACAGATATTTGGCTATCCGAGCACAAGTGGAGGAGATGATGATGATGATGATGAT

Db 1201 ATGATACAGATATTTGGCTATCCGAGCACAAGTGGAGGAGATGATGATGATGATGATGAT 1260  
 QY 1261 CTTGCTTATTTAGCGGAGATCGGAGCAGACATCTTTTGAGACATGCTATTCAATTGATA 1320  
 Db 1261 CTTGCTTATTTAGCGGAGATCGGAGCAGACATCTTTTGAGACATGCTATTCAATTGATA 1320  
 QY 1321 TCACCTGCCAGCGTGTCTCAAGACTTAATGGAAGAGAGAAATCTGCAAGGCTGATCTC 1380  
 Db 1321 TCACCTGCCAGCGTGTCTCAAGACTTAATGGAAGAGAGAAATCTGCAAGGCTGATCTC 1380  
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 Db 1381 GAGGAAGTCAGTGGCTCTATTGGATGCCAAATCTCGGCTCGGCTCTCCAGGAGCAA 1440  
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 Db 1441 CAAGAAAGATACATCACCTAGATTGGATCTCCTGCTGGAAGTCTCGAAGAAATGTA 1500  
 QY 1501 GTTGCAGCTCGAAAGTCACTAGTGCATTTGATCTGCTTCACAGGTTTCATAGTCTACTGG 1560  
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 Db 1561 TCTTGGAGGAGCAGATTTGGGGGGAACGGCTTGAATTTTGCAGTGCCTGCTTGTGTTA 1620  
 QY 1621 GTCTCCARAGAGACTTGTGTTCCGCGCATATTGCTGCTTCACGCACTGTTGCTGATTAGA 1680  
 Db 1621 GTCTCCARAGAGACTTGTGTTCCGCGCATATTGCTGCTTCACGCACTGTTGCTGATTAGA 1680  
 QY 1681 TTGGTCCAGGTCAGGAAATTTGCCGCTGCTGTTTATCTTCTGCTCATCGGTTGCCGGAGT 1740  
 Db 1681 TTGGTCCAGGTCAGGAAATTTGCCGCTGCTGTTTATCTTCTGCTCATCGGTTGCCGGAGT 1740  
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 Db 1741 CTGCTCCACGCGTGTATTGGCCGCAACCCCTATCTTTGTAACCATGGATAATGGATAGG 1800  
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 QY 1861 AAATGTTTCTACAACTTAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1912  
 Db 1861 AAATGTTTCTACAACTTAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 1912  
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 AAD02570  
 ID AAD02570 standard; cDNA; 1869 BP.  
 XX  
 AC AAD02570;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE Maize RuvB orthologue #5 cDNA.  
 KW Maize; RuvB orthologue; branch migration; heteroduplex extension;  
 KW homologous recombination; transformaton; transgenic plant; ss.  
 OS Zea mays.  
 XX  
 FH Key Location/Qualifiers  
 CDS 64..1380  
 FT /\*tag=a  
 FT /product= "Maize RuvB orthologue protein #5"  
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 PN WO200105975-A1.  
 XX  
 PD 25-JAN-2001.  
 XX  
 PF 13-JUN-2000; 2000WO-US16271.  
 XX



PR 16-JUL-1999; 99US-0144112.  
 XX (PION-) PIONEER HI-BRED INT INC.  
 XX Mahajan PB;  
 XX WPI: 2001-159537/16.  
 XX P-PSDB: AAY72566.  
 DR Novel maize RuvB nucleic acid useful for modulating levels of maize  
 PT RuvB in plants, as probes or amplification primers in the detection,  
 PT quantitation or isolation of gene transcripts -  
 XX  
 XX Claim 1; Page 80-82; 87pp; English.  
 XX The present sequence is a Zea mays RuvB orthologue #5 cDNA. RuvB along  
 CC with Ruva catalyses the branch migration process, also known as  
 CC heteroduplex extension, in homologous recombination. RuvB is used for  
 CC the control of homologous recombination or transformation efficiency in  
 CC transgenic plants. The RuvB nucleotide may be used as probes or  
 CC amplification primers for detecting, quantifying or isolating gene  
 CC transcripts, in detecting deficiencies in the mRNA level during screening  
 CC for desired transgenic plants, for detecting gene mutations, for  
 CC monitoring upregulation of expression or changes in enzyme activity, for  
 CC detecting any number of allelic variants, orthologues or paralogues of  
 CC the gene, or for site directed mutagenesis in eukaryotic cells. It may  
 CC also be used for recombinant expression of its encoded polypeptide, or  
 CC for use as immunogen in preparing and/or screening of antibodies, and in  
 CC sense or antisense suppression of one or more genes in a host cell,  
 CC tissue or plant. The RuvB proteins may be used in assays to agonise or  
 CC antagonise the enzyme function, or as immunogens or antigens for  
 CC screening antibodies.  
 XX  
 XX Sequence 1869 BP; 539 A; 373 C; 486 G; 471 T; 0 other;  
 Query Match 56.5%; Score 1080; DB 22; Length 1869;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1130; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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 DB 256 GGCATAGCCAGGAGCTCGGAGCAAGGTCCTTCTCTCTATGGTAGGATCAGAAGTG 315  
 QY 397 TACTCTCGGAGGTCAGAAAACACTGAGTGCTGATGAAAATTTCCGTAGAGCTATAGGT 456  
 DB 316 TACTCTCGGAGGTCAGAAAACACTGAGTGCTGATGAAAATTTCCGTAGAGCTATAGGT 375  
 QY 457 TTGCGGTATAAGGAAAACAAAGAGGTTTATCAAGGAGAGGTTACTGAACCTTCCCGAGAA 516  
 DB 376 TTGCGGTATAAGGAAAACAAAGAGGTTTATCAAGGAGAGGTTACTGAACCTTCCCGAGAA 435  
 QY 517 GAGGCTGAGACTACAACTGGTGGATATGCAAAAAGCAATAGCCATGTAATCATCAGCTTA 576  
 DB 436 GAGGCTGAGACTACAACTGGTGGATATGCAAAAAGCAATAGCCATGTAATCATCAGCTTA 495  
 QY 577 AAGAGCTGTTAAAGGAGCTAAGCAACTGAAGTTAGATTCTTCAATTTATGATGCTCTGATC 636  
 DB 496 AAGAGCTGTTAAAGGAGCTAAGCAACTGAAGTTAGATTCTTCAATTTATGATGCTCTGATC 555  
 QY 637 AAGGAAAAGGTGGCAGTGGGTGATGTTATATACATCGAAGCAAAATAGTGGAGCAGTCAAA 696  
 DB 556 AAGGAAAAGGTGGCAGTGGGTGATGTTATATACATCGAAGCAAAATAGTGGAGCAGTCAAA 615  
 QY 697 AGAGTTGCTAGATGCTGATTTCTTCTACAGATACGATCTTGAAGCTGAAGAGTATGTT 756  
 DB 616 AGAGTTGCTAGATGCTGATTTCTTCTACAGATACGATCTTGAAGCTGAAGAGTATGTT 675  
 QY 757 CCTATCCCAAGAGTGAAGTCCATAAGAAAAAGAAATTTGTCAGGATGTCACACTTCAT 816  
 DB 676 CCTATCCCAAGAGTGAAGTCCATAAGAAAAAGAAATTTGTCAGGATGTCACACTTCAT 735  
 QY 817 GACCTTGATGAGCAAAATGCTCAGCCCAAGGTGGCCCAAGATATTTGTCCTTATGGC 876

DB 736 GACCTTGATGAGCAAAATGCTCAGCCACAAGGTGGCCCAAGATATTTTGTCCCTTAAGGC 795  
 QY 877 CAGATGATGAACACCAAGAAAGACTGAAATCACCAGAAACTACCCCAAGAAATTAATAAG 936  
 DB 796 CAGATGATGAACACCAAGAAAGACTGAAATCACCAGAAACTACCCCAAGAAATTAATAAG 855  
 QY 937 GTGGTAAATAGATATATCGATGAAGGAATTCAGAGAGCTTTGACCTGGTGTGTTGTTCAAT 996  
 DB 856 GTGGTAAATAGATATATCGATGAAGGAATTCAGAGAGCTTTGACCTGGTGTGTTGTTCAAT 915  
 QY 997 GATGAGTCCACATGTTGGATATCGAATGTTTCTTATCTTAACCGTGCATGAGAGC 1056  
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 QY 1117 GATATGACAAGTCCACATGTTACCGGTGGATCTTCTAGATAGGCTGGTATTATTCGG 1176  
 DB 1036 GATATGACAAGTCCACATGTTACCGGTGGATCTTCTAGATAGGCTGGTATTATTCGG 1095  
 QY 1177 ACAGAGACATATGGCCCTACTGAGATGATACAGATATGGCTATCCGACCAAGTGGAG 1236  
 DB 1096 ACAGAGACATATGGCCCTACTGAGATGATACAGATATGGCTATCCGACCAAGTGGAG 1155  
 QY 1237 GAGATTGATGATGATGAAGAAAGTCTTGGCTTATTTAGGCGAGATCGGACGACAGACATCT 1296  
 DB 1156 GAGATTGATGATGATGAAGAAAGTCTTGGCTTATTTAGGCGAGATCGGACGACAGACATCT 1215  
 QY 1297 TTGAGACATGCTTATCAATTTGATATCACCTGCCAGCGTGGTCTCAAGACTAATGGAAGA 1356  
 DB 1216 TTGAGACATGCTTATCAATTTGATATCACCTGCCAGCGTGGTCTCAAGACTAATGGAAGA 1275  
 QY 1357 GAGAAAATCTGCAAGCTGATCTCGAGGAAGTCACTGGGCTCTATTGGATGCCAAATCC 1416  
 DB 1276 GAGAAAATCTGCAAGCTGATCTCGAGGAAGTCACTGGGCTCTATTGGATGCCAAATCC 1335  
 QY 1417 TCGGCTCGGCTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGATTGG 1467  
 DB 1336 TCGGCTCGGCTGCTCCAGGAGCAACAAGAAAGATACATCACCTAGATTGG 1386  
 RESULT 3  
 AAD02566  
 ID AAD02566 standard; cDNA; 1845 BP.  
 XX  
 AC AAD02566;  
 XX  
 DT 02-MAY-2001 (first entry)  
 XX  
 DE Maize RuvB orthologue #1 cDNA.  
 XX  
 KW Maize; RuvB orthologue; branch migration; heteroduplex extension;  
 KW homologous recombination; transformatio; transgenic plant; ss.  
 XX  
 OS Zea mays.  
 XX  
 FH Key  
 FT CDS  
 FT Location/Qualifiers  
 FT 85..1452  
 FT /tag= a  
 FT /product= "Maize RuvB orthologue protein #1"  
 XX  
 PN WO200105975-A1.  
 XX  
 PD 25-JAN-2001.  
 XX  
 PF 13-JUN-2000; 2000WO-US16271.  
 XX  
 PR 16-JUL-1999; 99US-0144112.  
 XX  
 PA (PION-) PIONEER HI-BRED INT INC.  
 XX

PI Mahajan PB;  
XX WPI: 2001-159537/16.  
DR P-PSDB: AAV72562.  
XX  
XX Novel maize RuvB nucleic acid useful for modulating levels of maize  
PT RuvB in plants, as probes or amplification primers in the detection,  
PT quantitation or isolation of gene transcripts -  
XX  
XX Claim 1: Page 67-69; 87pp; English.  
XX  
CC The present sequence is a Zea mays RuvB orthologue #1 cDNA. RuvB along  
CC with RuvA catalyses the branch migration process, also known as  
CC heteroduplex extension, in homologous recombination. RuvB is used for  
CC the control of homologous recombination or transformation efficiency in  
CC transgenic plants. The RuvB nucleotide may be used as probes or  
CC amplification primers for detecting, quantifying or isolating gene  
CC transcripts, in detecting deficiencies in the mRNA level during screening  
CC for desired transgenic plants, for detecting gene mutations, for  
CC monitoring upregulation of expression or changes in enzyme activity, for  
CC detecting any number of allelic variants, orthologues or paralogues of  
CC the gene, or for site directed mutagenesis in eukaryotic cells. It may  
CC also be used for recombinant expression of its encoded polypeptide, or  
CC for use as immunogen in preparing and/or screening of antibodies, and in  
CC sense or antisense suppression of one or more genes in a host cell,  
CC tissue or plant. The RuvB proteins may be used in assays to agonise or  
CC antagonise the enzyme function, or as immunogens or antigens for  
CC screening antibodies.  
XX  
SQ • Sequence 1845 BP; 530 A; 378 C; 490 G; 445 T; 2 other;

Query Match 30.1%; Score 576; DB 22; Length 1845;  
Best Local Similarity 98.8%; Pred. No. 6.5e-214;  
Matches 1426; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 84 GTTGGCGCGATGAGGATCGAGAGGTGCGATCGACCTCGAAGAGAGCGGATCGCCAC 143  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
75 GTTGGCGCGATGAGGATCGAGAGGTGCGATCGACCTCGAAGAGAGCGGATCGCCAC 134  
QY 144 CCACACCCACATCAAGGACTCGGCTCGACGCCAATGGGATGGGATTTGGTGGCGGC 203  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
135 CCACACCCACATCAAGGACTCGGCTCGACGCCAATGGGATGGGATTTGGTGGCGGC 194  
QY 204 GGGGTTGTTGGCGGAGCGGCGCGGAGCGCGCGGCTGGCGGTCGACATGATTCG 263  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
195 GGGGTTGTTGGCGGAGCGGCGGAGCGCGCGGCTGGCGGTCGACATGATTCG 254  
QY 264 CCAGAGAGAGATGGCGGCGGCGGCGGAGCGCGCGGCTGGCGGTCGACATGATTCG 323  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
255 CCAGAAAAAGATGGCGGCGGCGGCGGAGCGCGCGGCTGGCGGTCGACATGATTCG 314  
QY 324 GGGGTTGTTGGCGGATAGCGGAGCTCGGAGCAAGGTTCCTTCTGCTATGTT 383  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
315 GGGGTTGTTGGCGGATAGCGGAGCTCGGAGCAAGGTTCCTTCTGCTATGTT 374  
QY 384 AGGATCAGAGTGTACTCCTCGGAGGTCAAGAAACTGAGGTGCTGATGGAATTTCCG 443  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
375 AGGATCAGAGTGTACTCCTCGGAGGTCAAGAAACTGAGGTGCTGATGGAATTTCCG 434  
QY 444 TAGAGCTATAGGTTTGGGATATAGGAAACAAAGAGGTTTATGAAGGAGGTTACTGA 503  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
435 TAGAGCTATAGGTTTGGGATATAGGAAACAAAGAGGTTTATGAAGGAGGTTACTGA 494  
QY 504 ACTTTTCCAGAGAGGCTGAGAGTACAACTGGTGGATATGCAAAAAGCATTTAGCCATGT 563  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
495 ACTTTTCCAGAGAGGCTGAGAGTACAACTGGTGGATATGCAAAAAGCATTTAGCCATGT 554  
QY 564 AATCATCAGCTTAAAGACTGTTAAAGGAGCTAAGCAACTGAAGTTAGATTCTTCAATTTA 623  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
555 AATCATCAGCTTAAAGACTGTTAAAGGAGCTAAGCAACTGAAGTTAGATTCTTCAATTTA 614  
QY 624 TGATCCTCTGATCAAGGAAAGGTGGCAGTGGTGCATGTTATATACATCGAAGCAATAG 683  
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Job time : 289 secs